UNITED STATES PATENT AND TRADEMARK OFFICE

UNITED STATES DEPARTMENT OF COMMERCE
United States Patent and Trademark Office
Address: COMMISSIONER FOR PATENTS
P.O. Box 1450
Alexandria, Virginia 22313-1450
www.uspto.gov

APPLICATION NO.	FILING DATE	FIRST NAMED INVENTOR	ATTORNEY DOCKET NO.	CONFIRMATION NO.
10/792,176	03/02/2004	Brian T. Chait	016866-000211US	3757

20350 7590 04/30/2007

TOWNSEND AND TOWNSEND AND CREW, LLP
TWO EMBARCADERO CENTER
EIGHTH FLOOR
SAN FRANCISCO, CA 94111-3834

EXAMINER	
HA, JULIE	
ART UNIT	**PAPER NUMBER**
1654	

SHORTENED STATUTORY PERIOD OF RESPONSE	MAIL DATE	DELIVERY MODE
3 MONTHS	04/30/2007	PAPER

Please find below and/or attached an Office communication concerning this application or proceeding.

If NO period for reply is specified above, the maximum statutory period will apply and will expire 6 MONTHS from the mailing date of this communication.

Office Action Summary	Application No.	Applicant(s)	
	10/792,176	CHAIT ET AL.	
	Examiner	Art Unit	
	Julie Ha	1654	

-- The MAILING DATE of this communication appears on the cover sheet with the correspondence address --

Period for Reply

A SHORTENED STATUTORY PERIOD FOR REPLY IS SET TO EXPIRE 3 MONTH(S) OR THIRTY (30) DAYS, WHICHEVER IS LONGER, FROM THE MAILING DATE OF THIS COMMUNICATION.

- Extensions of time may be available under the provisions of 37 CFR 1.136(a). In no event, however, may a reply be timely filed after SIX (6) MONTHS from the mailing date of this communication.
- If NO period for reply is specified above, the maximum statutory period will apply and will expire SIX (6) MONTHS from the mailing date of this communication.
- Failure to reply within the set or extended period for reply will, by statute, cause the application to become ABANDONED (35 U.S.C. § 133). Any reply received by the Office later than three months after the mailing date of this communication, even if timely filed, may reduce any earned patent term adjustment. See 37 CFR 1.704(b).

Status

1)☒ Responsive to communication(s) filed on *20 March 2007*.

2a)☐ This action is **FINAL**. 2b)☒ This action is non-final.

3)☐ Since this application is in condition for allowance except for formal matters, prosecution as to the merits is closed in accordance with the practice under *Ex parte Quayle*, 1935 C.D. 11, 453 O.G. 213.

Disposition of Claims

4)☒ Claim(s) *64-74* is/are pending in the application.

4a) Of the above claim(s) _____ is/are withdrawn from consideration.

5)☐ Claim(s) _____ is/are allowed.

6)☒ Claim(s) *64-72 and 74* is/are rejected.

7)☒ Claim(s) *73* is/are objected to.

8)☐ Claim(s) _____ are subject to restriction and/or election requirement.

Application Papers

9)☐ The specification is objected to by the Examiner.

10)☐ The drawing(s) filed on _____ is/are: a)☐ accepted or b)☐ objected to by the Examiner.

Applicant may not request that any objection to the drawing(s) be held in abeyance. See 37 CFR 1.85(a).

Replacement drawing sheet(s) including the correction is required if the drawing(s) is objected to. See 37 CFR 1.121(d).

11)☐ The oath or declaration is objected to by the Examiner. Note the attached Office Action or form PTO-152.

Priority under 35 U.S.C. § 119

12)☐ Acknowledgment is made of a claim for foreign priority under 35 U.S.C. § 119(a)-(d) or (f).

a)☐ All b)☐ Some * c)☐ None of:

1.☐ Certified copies of the priority documents have been received.

2.☐ Certified copies of the priority documents have been received in Application No. _____.

3.☐ Copies of the certified copies of the priority documents have been received in this National Stage application from the International Bureau (PCT Rule 17.2(a)).

* See the attached detailed Office action for a list of the certified copies not received.

Attachment(s)

1) ☒ Notice of References Cited (PTO-892)
2) ☐ Notice of Draftsperson's Patent Drawing Review (PTO-948)
3) ☐ Information Disclosure Statement(s) (PTO/SB/08) Paper No(s)/Mail Date _____.
4) ☐ Interview Summary (PTO-413) Paper No(s)/Mail Date. _____ .
5) ☐ Notice of Informal Patent Application
6) ☐ Other: _____.

DETAILED ACTION

Amendment-After Non-Final Rejection filed on March 20, 2007 is acknowledged. Claims 64-74 are pending in this application. Claims 64-74 are examined on the merits in this office action.

Priority

1. The Applicants argue that the Examiner improperly denied priority to 07/891,177 priority date. Applicants claim priority from the '177 application through the corresponding PCT application WO 93/24834 ('834) filed on May 27, 1993. This is found persuasive and the Denial of Priority is withdrawn. The Current application has the priority date of May 27, 1993.

Withdrawn Rejections

2. The rejection of claim 73 under 35 U.S.C. 112, 2nd paragraph has been withdrawn in view of Applicants Amendment.

3. The rejection of claim 64, 71 and 72 under 35 U.S.C. 112, 1st paragraph, as failing to comply with the written description requirement is hereby withdrawn in view of Applicants arguments.

Maintained Rejection

Rejection-35 U.S.C. 102

4. The following is a quotation of the appropriate paragraphs of 35 U.S.C. 102 that form the basis for the rejections under this section made in this Office action:

> A person shall be entitled to a patent unless –
>
> (b) the invention was patented or described in a printed publication in this or a foreign country or in public use or on sale in this country, more than one year prior to the date of application for patent in the United States.

5. Claims 64 and 68 are rejected under 35 U.S.C. 102(b) as being anticipated by Tam JP (US Patent # 5144006).

6. The instant claims are drawn to a method for identifying a covalent modification of an amino acid residue in a polypeptide chain comprising detecting a mass difference between a formed polypeptide and a modified polypeptide by mass spectrometry, wherein the covalent modification is acetylation.

7. As described in the prior office action, Tam JP teaches a method for oxidative folding of peptide and protein substrates to form disulfide bonds using dimethyl sulfoxide and other equivalent sulfoxides as mild oxidizing agents. The reference teaches using 20% DMSO in aqueous solution as the oxidative folding reagent, the disulfide formation by the DMSO oxidation was rapid in all model peptides studies. A 50% conversion to the disulfide was found to be effected in about 5 to 30 minutes. The reaction was followed by analytical C18 reverse-phase HPLC for purification to give 32 to 45% overall yield. The integrity of each purified peptide was determined by Cf-252 fission ion mass spectrometry and the observed molecular mass was found to agree

with the calculated values (see column 4, lines 16-33 and Figure 5). This reads on claims 64 and 68.

Response to Arguments

8. Applicants argue that Tam (US Patent # 5144006) does not teach a "formed" polypeptide and thus is distinguishable from the rejected claims. This is not found persuasive because the specification discloses that covalent modifications on a polypeptide chain...polypeptides which are phosphorylated, acylated, glycosylated, cross-linked...referred as "modified polypeptides" (see paragraph [0087]). Modified polypeptides would be the same as formed polypeptide, since according to the specification, "formed polypeptide" is an existing polypeptide which is to be sequenced, thus modified polypeptides would be a "formed polypeptide" to be sequenced. The specification does not disclose that formed peptides cannot be modified peptides. The specification does not specify that "formed" and "modified" are independent from each other. For example, glycosylated peptide by the definition is a modified peptide. However, when it is awaiting to be sequenced, then it is also a formed peptide. Hence, the Tam et al meets the limitations of the "formed" peptide. Further, when two peptides are put into a solution, and the two peptides form a dipeptide, it would be considered a "formed peptide".

9. Claims 64, 66, 67, 70, 71 and 74 are rejected under 35 U.S.C. 102(b) as being anticipated by Hunt et al (Biomedical Mass Spectrometry, 1981, 8(9): 397-408).

10. The instant claims are drawn to a method for identifying a covalent modification of an amino acid residue wherein said mass spectrometry is quadrupole mass spectrometry.

11. As described in the prior office action, Hunt et al teach a new approach to the direct sequencing of oligopeptides in complex mixtures produced by enzymatic and acid hydrolysis of large protein segments and polypeptides in general. Mixtures of oligopeptides containing 2-8 residues are N-acetylated and N, O-permethylated and then volatilized directly into the ion source of a tandem or double analyzer mass spectrometer without fractionation by wet chemical or chromatographic steps (see p. 398, left column, lines 3-11). This reads on claims 64 and 66-67. The instrument employed is a Finnigan triple quadrupole mass spectrometer (see p. 398, left column, lines 36-37). This reads on claim 70. Furthermore, oligopeptide mixture analysis by collision activated dissociation can also be accomplished on the triple quadrupole with Q1, Q2, and Q3 operating in the RF, RF and RF-DC modes (see p. 398, right column, lines 29-32). Furthermore, under chemical ionization (CI) conditions when Leu and Ile residues occur at the N-terminus of oligopeptide, the collision activated dissociation mass spectrum of the $[A_1]^+$ sequence ion from Leu-Leu, Ile-Leu, Ile-Ala and Leu-Ala can be distinguished (see p. 405, right column, lines 18-23). This reads on claims 70-71 and 74.

Response to Arguments

12. Applicants argue that Hunt et al do not teach a "formed" polypeptide and formed polypeptides are polypeptides that are undergoing peptide ladder formation using the

chemistries provided in the specification. This is not found persuasive because the specification discloses that covalent modifications on a polypeptide chain...polypeptides which are phosphorylated, acylated, glycosylated, cross-linked...referred as "modified polypeptides" (see paragraph [0087]). Modified polypeptides would be the same as formed polypeptide, since according to the specification, "formed polypeptide" is an existing polypeptide which is to be sequenced, thus modified polypeptides would be a "formed polypeptide" to be sequenced. The specification does not disclose that formed peptides cannot be modified peptides. The specification does not specify that "formed" and "modified" are independent from each other. For example, glycosylated peptide by the definition is a modified peptide. However, when it is awaiting to be sequenced, then it is also a formed peptide. Hence, the Hunt et al meets the limitations of the "formed" peptide. Further, when two peptides are put into a solution, and the two peptides form a dipeptide, it would be considered a "formed peptide". In the instant case, Hunt et al teaches formed dipeptides and those peptides awaiting sequencing, thus it meets the limitation of "formed" peptide.

New Grounds for Rejection

Rejection-35 U.S.C. 102

13. The following is a quotation of the appropriate paragraphs of 35 U.S.C. 102 that form the basis for the rejections under this section made in this Office action:

A person shall be entitled to a patent unless –

(b) the invention was patented or described in a printed publication in this or a foreign country or in public use or on sale in this country, more than one year prior to the date of application for patent in the United States.

14. Claims 64 and 65 are rejected under 35 U.S.C. 102(b) as being anticipated by Beavis et al (Proc. Natl, Acad. Sci, 1990, 87: 6873-6877).

15. The instant claims are drawn to a method of identifying a covalent modification of an amino acid residue wherein the covalent modification is phosphorylation.

16. Beavis et al teach a method for determining the molecular masses of proteins in complex mixtures by mass spectrometry, wherein the method has the capacity to examine the components of mixtures without using any chromatographic separation steps and will tolerate relatively large amounts of buffers and inorganic contaminants (see abstract). This reads on claim 64. Further, the reference teaches that sinapinic acid has the property of being able to selectively ionize protein molecules in the presence of high concentrations of contaminating materials, such as lipids, carbohydrates and salts. It is also relatively nonselective in its behavior towards proteins of radically different primary structures and modifications, such as phosphorylation and glycosylation (see p. 6873, right column, 2nd paragraph). This reads on claim 65.

17. Claims 64 and 69 are rejected under 35 U.S.C. 102(b) as being anticipated by Cooks et al (Acc. Chem. Res., 1990, 23: 213-219) as evidenced by Hunt et al (Biomedical Mass Spectrometry, 1981, 8(9): 397-408) above.

18. The instant claims are drawn to a method for identifying a covalent modification of amino acid residues wherein said mass spectrometry is ion trap mass spectrometry.

19. Cooks et al teach that a sample of 10^8 molecules of a peptide can yield both a mass spectrum and MS/MS data, including structurally diagnostic sequence ions (see p.

214, left column, 2nd paragraph). The reference further teaches a cyclic peptide ionized by Cs+ SIMS; Figure 7 illustrates the structure of peptide and the fragmentation of the parent ions to yield sequence-specific daughters (see Figure 7 and paragraph 2, p. 218). Furthermore, as evidenced by Hunt et al, oligopeptide mixture analysis by collision activated dissociation can also be accomplished on the triple quadrupole with Q1, Q2, and Q3 operating in the RF, RF and RF-DC modes (see p. 398, right column, lines 29-32). Furthermore, under chemical ionization (CI) conditions when Leu and Ile residues occur at the N-terminus of oligopeptide, the collision activated dissociation mass spectrum of the $[A_1]^+$ sequence ion from Leu-Leu, Ile-Leu, Ile-Ala and Leu-Ala can be distinguished (see p. 405, right column, lines 18-23). Therefore, this reads on claims 64 and 69.

102(e) and 102(a)

> (e) the invention was described in (1) an application for patent, published under section 122(b), by another filed in the United States before the invention by the applicant for patent or (2) a patent granted on an application for patent by another filed in the United States before the invention by the applicant for patent, except that an international application filed under the treaty defined in section 351(a) shall have the effects for purposes of this subsection of an application filed in the United States only if the international application designated the United States and was published under Article 21(2) of such treaty in the English language.
>
> (a) the invention was known or used by others in this country, or patented or described in a printed publication in this or a foreign country, before the invention thereof by the applicant for a patent.

20. Claims 64 and 66 are rejected under 35 U.S.C. 102(e) as being anticipated by Coller BS (US Patent # 5328840).

21. The instant claims are drawn to a method for identifying a covalent modification of an amino acid residue in a polypeptide chain comprising detecting a mass difference

between a formed polypeptide and a modified polypeptide by mass spectrometry, wherein the covalent modification is acetylation.

22. Coller BS teaches a methodology of acetylating the amino terminus. Double coupling were performed with the phenylalanine in three of the syntheses and arginine in all of the syntheses. The amino acid terminus was acetylated while the peptide was still on the resin and fast atom bombardment mass spectrometry was performed on 2 of 5 peptides and demonstrated that the peptides has the expected mass (see column 24, lines 4-35). This meets the limitations of claims 64 and 66.

23. Claims 64 and 66 are rejected under 35 U.S.C. 102(a) as being anticipated by Coller BS as described above.

24. Claims 64 and 67 are rejected under 35 U.S.C. 102(e) as being anticipated by Stahl PD (US Patent # 5432260).

25. As described above, the claims are drawn to a method for identifying a covalent modification of an amino acid residue wherein the covalent modification is a glycosylation.

26. Stahl PD teaches the glycopeptides were synthesized in four steps and mannosylated peptides were purified by reverse-phase and ion-exchange chromatography (see column 9, lines 50-58). The purified peptides were then analyzed by amino acid analysis and mass spectrometry (see column 10, lines 21-23). Furthermore, identification and characterization of the glycopeptides was through amino acid analysis, mass spectrometry, Dionex carbohydrate chromatography system, and

fluorescamine analysis for free amines to verify structure (see column 10, lines 64-68). This meets the limitations of claims 64 and 67.

Response to Arguments

27. The Applicants argue that Stahl patent does not describe "formed" polypeptides and thus is distinguishable from the rejected claims. This is not found persuasive because the specification discloses that covalent modifications on a polypeptide chain...polypeptides which are phosphorylated, acylated, glycosylated, cross-linked...referred as "modified polypeptides" (see paragraph [0087]). Modified polypeptides would be the same as formed polypeptide, since according to the specification, "formed polypeptide" is an existing polypeptide which is to be sequenced, thus modified polypeptides would be a "formed polypeptide" to be sequenced. The specification does not disclose that formed peptides cannot be modified peptides. The specification does not specify that "formed" and "modified" are independent from each other. For example, glycosylated peptide by the definition is a modified peptide. However, when it is awaiting to be sequenced, then it is also a formed peptide. Hence, the Hunt et al meets the limitations of the "formed" peptide. In the instant case, Stahl patent teaches formed glycopeptides that were purified and then analyzed by amino acid analysis. Since the peptides are awaiting sequencing, this meets the limitation of "formed" peptide.

28. Claims 64 and 67 are rejected under 35 U.S.C. 102(a) as being anticipated by Stahl PD as described above.

Rejection-35 U.S.C. 103

29. The following is a quotation of 35 U.S.C. 103(a) which forms the basis for all obviousness rejections set forth in this Office action:

> (a) A patent may not be obtained though the invention is not identically disclosed or described as set forth in section 102 of this title, if the differences between the subject matter sought to be patented and the prior art are such that the subject matter as a whole would have been obvious at the time the invention was made to a person having ordinary skill in the art to which said subject matter pertains. Patentability shall not be negatived by the manner in which the invention was made.

30. The factual inquiries set forth in *Graham* **v.** *John Deere Co.*, 383 U.S. 1, 148 USPQ 459 (1966), that are applied for establishing a background for determining obviousness under 35 U.S.C. 103(a) are summarized as follows:

1. Determining the scope and contents of the prior art.
2. Ascertaining the differences between the prior art and the claims at issue.
3. Resolving the level of ordinary skill in the pertinent art.
4. Considering objective evidence present in the application indicating obviousness or nonobviousness.

31. This application currently names joint inventors. In considering patentability of the claims under 35 U.S.C. 103(a), the examiner presumes that the subject matter of the various claims was commonly owned at the time any inventions covered therein were made absent any evidence to the contrary. Applicant is advised of the obligation under 37 CFR 1.56 to point out the inventor and invention dates of each claim that was not commonly owned at the time a later invention was made in order for the examiner to consider the applicability of 35 U.S.C. 103(c) and potential 35 U.S.C. 102(e), (f) or (g) prior art under 35 U.S.C. 103(a).

32. Claims 64, 71-72 and 74 are rejected under 35 U.S.C. 103(a) as being unpatentable over Wellner D (US Patent # 5008372) in view of Hunt et al (Biomedical Mass Spectrometry, 1981, 8(9): 397-408).

33. The instant claims are drawn to a method for identifying a covalent modification of an amino acid residue in a polypeptide chain, producing reaction mixtures from the formed and modified polypeptide, each reaction mixture containing a peptide ladder comprising a series of adjacent polypeptides in which each member of the series differs from the next adjacent member by one amino acid residue, reacting the formed and modified polypeptide with a molar excess of a pair of reagents comprising a coupling reagents and a terminating reagent.

34. Wellner D teaches that an important method for determining the sequence of amino acids in proteins and peptides is known as the Edman degradation process. The process involves coupling the N-terminal amino acid of the protein or peptide in a basic environment to pheynylisothiocyanate (PITC) to form phenylthiocarbamyl (PTC) derivative, then cleaving the PTC derivative using anhydrous strong acid, such as trifluoroacetic acid, to form an anilinothiazolinone (ATZ) derivative of the N-terminal amino acid and free peptide which is the original protein or peptide with the N-terminal amino acid residue removed, then converting the ATZ amino acid derivative to a phenylthiohydantoin (PTH) amino acid derivative which can be analyzed by chromatograph (see column 1, lines 19-36). Since Edman degradation forms a covalent modification of the peptide and would form a peptide ladder (since cleaving one amino acid at a time), this reads on claim 64, 71-72 and 74. The differences between the reference and the instant claims are that the reference does not teach mass spectrometry analysis.

35. However, Hunt et al teach a new approach to the direct sequencing of oligopeptides in complex mixtures produced by enzymatic and acid hydrolysis of large protein segments and polypeptides in general. Mixtures of oligopeptides containing 2-8 residues are N-acetylated and N, O-permethylated and then volatilized directly into the ion source of a tandem or double analyzer mass spectrometer without fractionation by wet chemical or chromatographic steps (see p. 398, left column, lines 3-11). This reads on claims 64 and 72. The instrument employed is a Finnigan triple quadrupole mass spectrometer (see p. 398, left column, lines 36-37). Furthermore, oligopeptide mixture analysis by collision activated dissociation can also be accomplished on the triple quadrupole with Q1, Q2, and Q3 operating in the RF, RF and RF-DC modes (see p. 398, right column, lines 29-32). Furthermore, under chemical ionization (CI) conditions when Leu and Ile residues occur at the N-terminus of oligopeptide, the collision activated dissociation mass spectrum of the $[A_1]^+$ sequence ion from Leu-Leu, Ile-Leu, Ile-Ala and Leu-Ala can be distinguished (see p. 405, right column, lines 18-23 and Table 1 and Figure 11). Therefore, this reads on claim 64, 71-72 and 73 in part and 74.

36. Therefore, it would have been obvious for one of ordinary skill in the art to combine the technique of mass spectrometry to monitor the cleavage of amino acid to identify the specific modified amino acid from non-modified amino acid using the Edman degradation. There is a reasonable expectation of success since Hunt et al teach that the sequences of several large proteins have been determined using a combination of the automated Edman degradation and Biemann methodologies (using mass spectrometry) (see p. 397, right column, 1st paragraph). Hunt et al teach a method of

using mass spectrometry to ability to distinguish Asp-Asn and Glu-Gln amino acid pairs, using the mass spectrometry. Since Edman degradation peptides can be analyzed by mass spectrometry, there is a reasonable expectation of success to analyze the amino acid sequence information using the Hunt et al method and mass spectrometry.

37. Claims 64 and 71-72 and 74 are rejected under 35 U.S.C. 103(a) as being unpatentable over Merrifield RB (Journal of American Chemical Society, 1963, 85(14): 2149-2154) in view of Hunt et al (Biomedical Mass Spectrometry, 1981, 8(9): 397-408).

38. The instant claims are drawn to a method for identifying a covalent modification of an amino acid residue in a polypeptide chain, producing reaction mixtures from the formed and modified polypeptide, each reaction mixture containing a peptide ladder comprising a series of adjacent polypeptides in which each member of the series differs from the next adjacent member by one amino acid residue, reacting the formed and modified polypeptide with a molar excess of a pair of reagents comprising a coupling reagents and a terminating reagent.

39. Merrifield RB teaches peptide synthesis that is dependent on the attachment of the first amino acid of the chain to a solid polymer by a covalent bond, the addition of the succeeding amino acids one at a time in a stepwise manner until the desired sequence is assembled, and finally the removal of the peptide from the solid support (see p. 2149, left column, 2nd paragraph, Figure 1, p. 2150 and Figure 2, p. 2153). This reads on peptide ladder of claim 72, since Figure 1 shows a peptide ladder being formed and as the reference teaches that "the addition of the succeeding amino acids

one at a time in a stepwise manner until the desired sequence is assembled". The reference teaches that the intermediate peptides are purified, not by the usual recrystallization procedures, but by dissolving away the impurities...it will lend itself to automation and provide a route to the synthesis of some of the higher molecular weight polypeptides which have not been accessible by conventional procedures (see p. 2149, right column, 1st paragraph). This reads on claims 64, 71 and 74. The difference between the reference and the instant application is that the reference does not teach mass spectrometry.

40. As described supra, Hunt et al teach a new approach to the direct sequencing of oligopeptides in complex mixtures produced by enzymatic and acid hydrolysis of large protein segments and polypeptides in general. Mixtures of oligopeptides containing 2-8 residues are N-acetylated and N, O-permethylated and then volatilized directly into the ion source of a tandem or double analyzer mass spectrometer without fractionation by wet chemical or chromatographic steps (see p. 398, left column, lines 3-11). This reads on claims 64 and 72. The instrument employed is a Finnigan triple quadrupole mass spectrometer (see p. 398, left column, lines 36-37). Furthermore, oligopeptide mixture analysis by collision activated dissociation can also be accomplished on the triple quadrupole with Q1, Q2, and Q3 operating in the RF, RF and RF-DC modes (see p. 398, right column, lines 29-32). Furthermore, under chemical ionization (CI) conditions when Leu and Ile residues occur at the N-terminus of oligopeptide, the collision activated dissociation mass spectrum of the $[A_1]^+$ sequence ion from Leu-Leu, Ile-Leu,

Ile-Ala and Leu-Ala can be distinguished (see p. 405, right column, lines 18-23 and Table 1 and Figure 11). Therefore, this reads on claim 64, 71-72 and 73 in part and 74.

41. Therefore, it would have been obvious for one of ordinary skill in the art to combine the technique of mass spectrometry to monitor the peptide synthesis and identify the specific modified amino acid from non-modified amino acid using the Merrifield synthesis. There is a reasonable expectation of success since Hunt et al teach a method of using mass spectrometry to ability to distinguish Asp-Asn and Glu-Gln amino acid pairs, using the mass spectrometry. Since Hunt et al teaches different strategies that are employed to determine the primary structure of proteins and polypeptides by mass spectrometry (see 1st paragraph of Introduction) and that mass analysis of the fragment ions affords a conventional mass spectrum of the particular oligopeptide component passed through the first stage of the instrument (see last paragraph of Introduction (last 2 sentences)), there is a reasonable expectation of success to analyze the amino acid sequence information using the Hunt et al method and mass spectrometry.

Allowable Subject Matter

42. Claim 73 is objected to as being dependent upon a rejected base claim, but would be allowable if rewritten in independent form including all of the limitations of the base claim and any intervening claims.

Conclusion

43. Claim 73 is objected to as being dependent upon a rejected base claim, but would be allowable if rewritten in independent form including all of the limitations of the base claim and any intervening claims. Claims 64, 71-72 and 74 are rejected. No claims are allowed.

Any inquiry concerning this communication or earlier communications from the examiner should be directed to Julie Ha whose telephone number is 571-272-5982. The examiner can normally be reached on Mon-Fri, 8:00 am to 4:30 pm.

If attempts to reach the examiner by telephone are unsuccessful, the examiner's supervisor, Cecilia Tsang can be reached on 571-272-0562. The fax phone number for the organization where this application or proceeding is assigned is 571-273-8300.

Information regarding the status of an application may be obtained from the Patent Application Information Retrieval (PAIR) system. Status information for published applications may be obtained from either Private PAIR or Public PAIR. Status information for unpublished applications is available through Private PAIR only. For more information about the PAIR system, see http://pair-direct.uspto.gov. Should you have questions on access to the Private PAIR system, contact the Electronic Business Center (EBC) at 866-217-9197 (toll-free). If you would like assistance from a USPTO Customer Service Representative or access to the automated information system, call 800-786-9199 (IN USA OR CANADA) or 571-272-1000.

Julie Ha
Patent Examiner
AU 1654

4/11/07
ANISH GUPTA
PRIMARY EXAMINER